High-Resolution Analysis of Synaptic Proteins

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Challenge/Problem:

While work over the past decades has identified most of the proteins associated with synaptic vesicles and the molecular pathway that underlies synaptic transmission, so far it has not been possible to obtain quantitative information (e.g. copy number) about the proteins present.

Progress:

We have developed our method and applied it to quantify the integral membrane proteins on synaptic vesicles, including the H^+/ATPase, synaptic vesicle protein 2, synaptophysin, synaptotagmin, synaptobrevin, synaptogyrin, and the glutamate transporters.

Approach:

Our method is based on single-molecule total-internal-reflection-fluorescence (TIRF) microscopy, microfluidics, and statistical de-convolution for ascertaining the absolute number of membrane proteins on individual synaptic vesicles.

Current/Near Term Products:

Two lines of near-term products are: (1) A highly sensitive single-molecule imaging and statistical de-convolution technique for quantifying proteins on synaptic vesicles, and (2) Provide the first quantitative measurement on the number of proteins on synaptic vesicles to the neuroscience community.

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Future Plans:

Future plans include utilizing the high-resolution single-molecule imaging and statistical de-convolution techniques we developed for quantifying proteins in different synaptic systems, and studying changes in protein targeting in genetically manipulated model organisms.

Keywords: **Synaptic Vesicles, Synaptic Proteins, Single-Molecule Imaging, Quantitative Biology**